AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions and listings of all claims in the application.

1-9 (Cancelled)

10. (New) A method for generating a at least one non-naturally occurring variant protein with at least one desired characteristic relative to a scaffold protein, said method comprising:

a) inputting into a computer a primary library comprising a plurality of first protein sequences and said scaffold protein sequence;

b) aligning said plurality of first protein sequences and said scaffold protein sequence to generate an alignment of sequences having variable residue positions, said alignment generated using an alignment program on said computer;

c) analyzing said alignment to generate a probability distribution of amino acid residues at teach variable residue position, such that each variable residue position has a set of possible amino acids;

d) combining amino acid residues from said probability distribution at a plurality of variable positions to generate a secondary library of secondary sequences;

e) computationally ranking said secondary library and eliminating at least one unfavorably ranked sequence from said secondary library to generate a tertiary library, wherein at least one sequence of said tertiary library is different from said primary sequences; and

f) screening said tertiary library to identify at least one non-naturally occurring variant protein with said desired characteristic.

11. (New) A method according to claim 10, wherein said step of screening said tertiary library comprises synthesizing a plurality of sequences in said tertiary library.

12. (New) A method according to claim 11, wherein said synthesizing is done by multiple PCR with pooled oligonucleotides.

13. (New) A method according to 11, wherein said pooled oligonucleotides are added in equimolar amounts.

14. (New) A method according to claim 11, wherein said pooled oligonucleotides are added in amounts that correspond to the frequency of the amino acid residues from said probability distribution.

15. (New) A method according to claim 12, wherein said pooled oligonucleotides are pooled in relative amounts.